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AMENDMENTS TO THE SPECIFICATION

SEQUENCE LISTING

Sequence Name: SEQ ID NO:1
Length: 1737 base pairs
Type: DNA

atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc	60
cggaggggtgc tgaccatcgc cttcgccctg ctcacacctg gcctcatgac ctgggcctac	120
gccgcggggg tgccgctggc ctcgatcgc tacggcctcc tggccttcgg cctctacggg	180
gccttccttt cagcgcacct ggtggcgag agcctcttcg cgtacctgga gcaccggcgg	240
gtggcgggcg cggcggggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc	300
atctccgcct accaggagga ccccgcgta ctcgcccagt gcctggcgtc cgcccgcgcc	360
ctgctgtacc cgcgcgcgcg gctgcgcgct ctcattggtg tggatggcaa ccgcgccgag	420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggacct cgccacgtac	480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cgcggggcgc ggtgggcgcc	540
ggagcctatc gggaggtgga ggcgaggat cctggggcgc tggcagtgga ggcgctggtg	600
aggactcgca ggtgcgtgtg cgtggcgag cgctggggcg gcaagcgca ggtcatgtac	660
acagccttca agcgctcgg agattcgggt gactacgtgc aggtctgtga ctcgacaca	720
aggttggacc ccattggcact gctggagctc gtgcgggtac tggacgagga ccccgggta	780
ggggctgttg gtggggacgt gcggatcctt aaccctctgg actcctgggt cagcttccta	840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttcac	900
tgtgtatcct gcatcagcgg tcctctaggc ctatatagga ataacctctt gcagcagttt	960
cttgaggcct ggtacaacca gaagtctctg ggtaccact gtacttttgg ggatgaccgg	1020
cacctacca accgatgct cagcatgggt tatgtacca agtacacctc caggctccgc	1080
tgctactcag agacgcctc gtccttctg cggtagctga gccagcagac acgctggtcc	1140
aagtcgtact tccgtgagt gctgtacaac gcgctctggt ggcaccggca ccatgcgtgg	1200
atgacctacg aggcggtggt ctcggcctg tccccctct tcgtggcggc cactgtgctg	1260
cgtctgttct acgcggggcg cccttggggc ctgctgtggg tgcgtgctgt cgtgcagggc	1320
gtggcactgg ccaaggcggc cttcgcgcc tggctgcggg gctgcctgcg catggtgctt	1380
ctgtcgtctc acgcgcccct ctacatgtgt ggctcctgc ctgccaagtt cctggcgcta	1440
gtcaccatga accagagtgg ctggggcacc tcgggcgggc ggaagctggc cgctaactac	1500
gtccctctgc tgccctggc gctctggggc ctgctgctgc ttgggggcct ggtccgcagc	1560

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gtagcacacg aggccagggc cgactggagc ggcccttccc gcgcagccga ggcctaccac 1620
ttggccgcgg gggccggcgc ctacgtgggc tactgggtgg ccatgttgac gctgtactgg 1680
gtgggcgtgc ggaggctttg cggcgggcgg accgggggct accgcgtcca ggtgtga 1737

Sequence Name: SEQ ID NO:2
Length: 578 amino acids
Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg
65 70 75 80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

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Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Pro Leu Gly Leu Tyr Arg Asn Asn Leu Leu Gln Gln Phe
305 310 315 320

Leu Glu Ala Trp Tyr Asn Gln Lys Phe Leu Gly Thr His Cys Thr Phe
325 330 335

Gly Asp Asp Arg His Leu Thr Asn Arg Met Leu Ser Met Gly Tyr Ala
340 345 350

Thr Lys Tyr Thr Ser Arg Ser Arg Cys Tyr Ser Glu Thr Pro Ser Ser
355 360 365

Phe Leu Arg Trp Leu Ser Gln Gln Thr Arg Trp Ser Lys Ser Tyr Phe
370 375 380

Arg Glu Trp Leu Tyr Asn Ala Leu Trp Trp His Arg His His Ala Trp
385 390 395 400

Met Thr Tyr Glu Ala Val Val Ser Gly Leu Phe Pro Phe Phe Val Ala
405 410 415

Ala Thr Val Leu Arg Leu Phe Tyr Ala Gly Arg Pro Trp Ala Leu Leu
420 425 430

Trp Val Leu Leu Cys Val Gln Gly Val Ala Leu Ala Lys Ala Ala Phe

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435

440

445

Ala Ala Trp Leu Arg Gly Cys Leu Arg Met Val Leu Leu Ser Leu Tyr
450 455 460

Ala Pro Leu Tyr Met Cys Gly Leu Leu Pro Ala Lys Phe Leu Ala Leu
465 470 475 480

Val Thr Met Asn Gln Ser Gly Trp Gly Thr Ser Gly Arg Arg Lys Leu
485 490 495

Ala Ala Asn Tyr Val Pro Leu Leu Pro Leu Ala Leu Trp Ala Leu Leu
500 505 510

Leu Leu Gly Gly Leu Val Arg Ser Val Ala His Glu Ala Arg Ala Asp
515 520 525

Trp Ser Gly Pro Ser Arg Ala Ala Glu Ala Tyr His Leu Ala Ala Gly
530 535 540

Ala Gly Ala Tyr Val Gly Tyr Trp Val Ala Met Leu Thr Leu Tyr Trp
545 550 555 560

Val Gly Val Arg Arg Leu Cys Arg Arg Arg Thr Gly Gly Tyr Arg Val
565 570 575

Gln Val

Sequence Name: SEQ ID NO:3
Length: 1071 base pairs
Type: DNA

atgagacagc aggacgcgcc caagcccaact cctgcagccc gccgctgctc cggcctggcc 60
cggagggtgc tgaccatcgc cttcgccctg ctcatacttg gccatcatgac ctgggcctac 120
gccgcggggg tgccgctggc ctcgatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttccttt cagcgacact ggtggcgag agcctcttcg cgtacctgga gcaccggcg 240
gtggcgggcg cggcggggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccggtac ctgcgccagt gcctggcgctc cgcccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgct ctcattgttg tggatggcaa ccgcgccgag 420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggaccc cgccacgtac 480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cggcggggcg ggtggggcgc 540

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```
ggagcctatc gggaggtgga ggcggaggat cctgggcggc tggcagtgga ggcgctggtg 600
aggactcgca ggtgctgttg cgtggcgagc cgctggggcg gcaagcgaga ggtcatgtac 660
acagccttca aggcgctcgg agattcgggtg gactacgtgc aggtctgtga ctcgacaca 720
aggttggacc ccatggcact gctggagctc gtgcgggtac tggacgagga cccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aaccctctgg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttccac 900
tgtgtatcct gcatcagcgg ttctctaggt acacctccag gtcccgtgc tactcagaga 960
cgccctcgtc cttctgcggg tggctgagcc agcagacacg ctgggtccaag tcgtacttcc 1020
gtgagtggct gtacaacgcg ctctggtggc accggcacca tgcgtggatg a 1071
```

Sequence Name: SEQ ID NO:4

Length: 376 amino acids

Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg
65 70 75 80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

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Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Ser Leu Gly Thr Pro Pro Gly Pro Ala Ala Thr Gln Arg
305 310 315 320

Arg Pro Arg Pro Ser Cys Gly Gly Ala Ser Arg His Ala Gly Pro Ser
325 330 335

Arg Thr Ser Val Ser Gly Cys Thr Thr Arg Ser Gly Gly Thr Gly Thr
340 345 350

Met Arg Gly Pro Thr Arg Arg Trp Ser Pro Ala Cys Ser Pro Ser Ser
355 360 365

Trp Arg Pro Leu Cys Cys Val Cys
370 375

Sequence Name: SEQ ID NO:5
Length: 1083 base pairs
Type: DNA

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```
atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc 60
cggaggggtgc tgaccatcgc cttcgccctg ctcacccctg gcctcatgac ctgggcctac 120
gccgcggggg tgccgctggc ctcgcatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttccttt cagcgcacct ggtggcgagc agcctcttcg cgtacctgga gcaccggcgg 240
gtggcgggcg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccgcgtag ctgcgccagt gcctggcgct cggccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgct ctcattggtg tggatggcaa ccgcgcgcgag 420
gacctctaca tggctgacat gttccgcgag gtcttcgctg acgaggacct cgccacgtac 480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cggcgggcgc ggtgggcgcc 540
ggagcctatc gggaggtgga ggcggaggat cctgggcggc tggcagtgga ggcgctggtg 600
aggactcgca ggtgcgtgtg cgtggcgagc cgctggggcg gcaagcgca ggtcatgtac 660
acagccttca aggcgctcgg agattcgggt gactacgtgc aggtctgtga ctcgacaca 720
aggttggaac ccatggcact gctggagctc gtgcgggtac tggacgagga ccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aaccctctgg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttcac 900
tgtgtatcct gcacagcgg tcctctagaa tcctgccag gccccagga gcacgcgatg 960
atgccctcat tcctgcgcc cgtgcaggta cacctccagg tcccgctgct actcagagac 1020
gccctcgtcc tcctgcgggt ggctgagcca gcagacacgc tggccaagt cgtacttcg 1080
tga \ 1083
```

Sequence Name: SEQ ID NO:6
Length: 360 amino acids
Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg

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65

70

75

80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Pro Leu Glu Ser Cys Pro Gly Pro Arg Glu His Ala Met
305 310 315 320

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Met Pro Ser Phe Leu Ala Pro Val Gln Val His Leu Gln Val Pro Leu
325 330 335

Leu Leu Arg Asp Ala Leu Val Leu Pro Ala Val Ala Glu Pro Ala Asp
340 345 350

Thr Leu Val Gln Val Val Leu Pro
355 360

Sequence Name: SEQ ID NO:7
Length: 1065 base pairs
Type: DNA

```
atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc 60
cggagggtgc tgaccatcgc cttcgccctg ctcatcctgg gcctcatgac ctgggcctac 120
gccgcggggg tgccgctggc ctccgatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttctttt cagcgcacct ggtggcgagc agcctcttcg cgtacctgga gcaccggcgg 240
gtggcgggcg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccgcgtag ctgcgccagt gcctggcgtc cgcccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgtc ctcatggtgg tggatggcaa ccgcgccgag 420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggaccc cgccacgtac 480
gtgtggggacg gcaactacca ccagccctgg gaaccgcggc cggcgggcgc ggtggggcgc 540
ggagcctatc gggagggtga ggcggaggat cctggggcggc tggcagtga ggcgctggtg 600
aggactcgca ggtgcgtgtg cgtggcgagc cgctggggcg gcaagcgca ggtcatgtac 660
acagccttca aggcgctcgg agattcgggt gactacgtgc aggtctgtga ctggacaca 720
aggttggaac coattggcact gctggagctc gtgcgggtac tggacgagga cccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aacctcttgg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttcac 900
tgtgtatcct gcatcagcgg tcctctagga ctatatagga ataacctctt gcagcagttt 960
cttgaggcct ggtacaacca gaagttcctg ggtaccact gtacttttgg ggatgaccgg 1020
cacctacca accgcatgct cagcatgggt tatgtacca agtaa 1065
```

Sequence Name: SEQ ID NO:8
Length: 320 amino acids
Type: PRT

Ala Phe Leu Ser Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu
1 5 10 15

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Glu His Arg Arg Val Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala
20 25 30

Thr Ala Arg Ser Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro
35 40 45

Ala Tyr Leu Arg Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro
50 55 60

Arg Ala Arg Leu Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu
65 70 75 80

Asp Leu Tyr Met Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp
85 90 95

Pro Ala Thr Tyr Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro
100 105 110

Ala Ala Ala Gly Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala
115 120 125

Glu Asp Pro Gly Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg
130 135 140

Cys Val Cys Val Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr
145 150 155 160

Thr Ala Phe Lys Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys
165 170 175

Asp Ser Asp Thr Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg
180 185 190

Val Leu Asp Glu Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg
195 200 205

Ile Leu Asn Pro Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg
210 215 220

Tyr Trp Val Ala Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His
225 230 235 240

Cys Val Ser Cys Ile Ser Gly Pro Leu Gly Leu Tyr Arg Asn Asn Leu
245 250 255

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Leu Gln Gln Phe Leu Glu Ala Trp Tyr Asn Gln Lys Phe Leu Gly Thr
260 265 270

His Cys Thr Phe Gly Asp Asp Arg His Leu Thr Asn Arg Met Leu Ser
275 280 285

Met Gly Tyr Ala Thr Lys Ala Glu Gly Thr Arg Trp Ser Gly Thr Pro
290 295 300

Pro Gly Pro Ala Ala Thr Gln Arg Arg Pro Arg Pro Ser Cys Gly Gly
305 310 315 320

Sequence Name: SEQ ID NO:9
Length: 20 base pairs
Type: DNA

cgggcttgctc agagctactt 20

Sequence Name: SEQ ID NO:10
Length: 20 base pairs
Type: DNA

agggcgtctc tgagtagcag 20

Sequence Name: SEQ ID NO:11
Length: 20 base pairs
Type: DNA

gcctcatctg tggagatggt 20

Sequence Name: SEQ ID NO:12
Length: 20 base pairs
Type: DNA

tcccagaggt ccactaatgc 20

Sequence Name: SEQ ID NO:13
Length: 20 base pairs
Type: DNA

catccaggtg tgcgactctg 20

Sequence Name: SEQ ID NO:14
Length: 20 base pairs
Type: DNA

cgctgctcag gaaggaaatc 20

Sequence Name: SEQ ID NO:15
Length: 2068
Type: DNA

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gtaagctgag gggaccaggt ggtcgatgtg tggaggccaa tgaatatacct agcgtgtgtg 60
catgctgaga gttctccaaa tccaaagtaa ctcaccagac aatgggctct atcaagttag 120
acttttagagg agagaggagg ataccataat gggcagagg gccatttgca ttgagccaat 180
ggactctacc aagttagata ttagggaaga ggggaagata ctataaggga caaggctggc 240
atttgcattg aaccatggaa tgcggtgaac tctaccaaga gaggaagag ggtagagaat 300
tccacctaga attgagatag gagtgtgttc tgtcatggag accaaggtag cacagtggg 360
agtgaagtag gaagggcaag agacaaatgg atagagtggg atctaactag tgagagagcc 420
acggagaaag aaacaagtga gagaagagga gcacctgaac tctagtaagt tcttcaagag 480
aagacaagta attccatgag actcagggga ggatgatcta gaccaagtga agttcaggg 540
agagtgattt ctgcaagcc aggtccactg aaataccag aggaaacttg ggataatcca 600
ggggaatcca tgcattaatt cactcaaaa atattcacta ggtgcctaga atgtttaagc 660
tgcggggata cagcaatagg cagacaggac accaattgat tacatcagtt ggggagacac 720
acaagaaata aataagtaga acatacagta tgttcatgat atgtgttatg gagataaata 780
atgccgggca aggggtgttg ataggaagtt ttgggggttg ggtgaagtg ttaagtggag 840
tgctgaagg atggggctca aggctgagaa tagtgtggct ggagcactga actgggggag 900
tattaggaga gcaggatgga gagttaagga gtgggtccact catgaaaggc ttataggtct 960
aaggactctg actaagatga gggagccatg ggagggtttt aagcagagaa gtgacacgtt 1020
gtaatgggat ccctctggca gccgttttgg gtacagacta caaaaggcaa ggtcgggaagc 1080
agggaggcca ctgaggatgc caagtgcac aggggaagga gtctggacac tgtcaagtaa 1140
tgcccaggat tctcctcttg tgtgggcttg gctggaaacc atgcaggat tgattaatga 1200
tgtctgccac aaaacaggaa ggaggcctga tggttccctt gagaagttct aatacataga 1260
ctaccctggg tagcaaccac acccatcttg ctccctcccta ggctgccag taataaagca 1320
tggtagtatt agtaatatgt tagtgatagt attagtaata gtgtcagtaa ccaacatgat 1380
attagtaaca gcaatagtaa ttgtaacagc aatagtcata gtaaaaacgg tagtagctaa 1440
catttattga gaaataacta tctactggtc ctaagcactt ggcgtttaat ttcattcaat 1500
ccttactatc ctgtcttat gagagccttt tttttttct tatagagtct tgctgtgttg 1560
ctcaggctca ggctggagtg caggggcacg atcatggctc actgcagcct caaactcctg 1620
agctcaagtg attccccat ctcagcctcc caaatagctg ggactacag ccaccagcc 1680
cggctaattt tttttttttt ttttttttt tagagatggg gtctcactat gttgcctagg 1740
ctgatctcaa actcttagcc tcaagtgatc ccctacctc agcctcctaa agtgctggga 1800

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ttacaggcat gagccattgc atcccaccca ttggtgctta tttatttatt tattttattta 1860

tttagagatg gggctcttgc atgttgccca ggctggtctt gaactcctta tccctcagcc 1920

tcccaaagtg ctgggattac aggagtgagc caccgcgtcc aggcctagga accattatcc 1980

accctattct acacatgaga aactgagggc ctagagaggt taagaaactc gccccagtg 2040

gccgtccaca gtggtcattt ctgcctcc 2068

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AMENDMENTS TO THE SPECIFICATION

SEQUENCE LISTING

Sequence Name: SEQ ID NO:1
Length: 1737 base pairs
Type: DNA

atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc	60
cggaggggtgc tgaccatcgc cttcgccctg ctccatcttg gcctcatgac ctgggcctac	120
gccgcggggg tgccgctggc ctccgatcgc tacggcctcc tggccttcgg cctctacggg	180
gccttccttt cagcgcacct ggtggcgcag agcctcttcg cgtacctgga gcaccggcgg	240
gtggcggcgg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc	300
atctccgcct accaggagga ccccgcgtag ctgcgccagt gcctggcgtc cgcccgcgcc	360
ctgctgtacc cgcgcgcgcg gctgcgcgct ctcatggtgg tggatggcaa ccgcgccgag	420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggaccc cgccacgtac	480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cggcggggcg ggtgggcgcc	540
ggagcctatc gggaggtgga ggcggaggat cctgggcggc tggcagtgga ggcgctggtg	600
aggactcgca ggtgcgtgtg cgtggcgcag cgctggggcg gcaagcgca ggtcatgtac	660
acagccttca aggcgctcgg agattcgggt gactacgtgc aggtctgtga ctcgacaca	720
aggttggacc ccatggcact gctggagctc gtgcgggtac tggacgagga cccccgggta	780
ggggctgttg gtggggacgt gcggatcctt aaccctctgg actcctgggt cagcttccta	840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttccac	900
tgtgtatcct gcatcagcgg tctctaggc ctatatagga ataacctctt gcagcagttt	960
cttgaggcct ggtacaacca gaagttcctg ggtaccact gtacttttgg ggatgaccgg	1020
cacctacca accgcatgct cagcatgggt tatgtacca agtacacct caggccccgc	1080
tgctactcag agacgccctc gtccttcctg cggcggctga gccagcagac acgctggtcc	1140
aagtcgtact tccgtgagtg gctgtacaac gcgctctggt ggcaccggca ccatgcgtgg	1200
atgacctacg aggcgggtgt ctccggcctg tccccctct tcgtggcggc cactgtgctg	1260
cgtctgttct acgcggggcg cccttggggc ctgctgtggg tgctgctgtg cgtgcagggc	1320
gtggcactgg ccaaggcggc cttcgcggcc tggctgcggg gctgcctgcg catggtgctt	1380
ctgtcgctct acgcgccct ctacatgtgt ggcctcctgc ctgccaagtt cctggcgcta	1440
gtcaccatga accagagtgg ctggggcacc tcgggccggc ggaagctggc cgctaactac	1500
gtccctctgc tgcccctggc gctctgggcg ctgctgctgc ttgggggcct ggtccgcagc	1560

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gtagcacacg aggccagggc cgactggagc ggcccttccc gcgcagccga ggcctaccac 1620
ttggccgcgg gggccggcgc ctacgtgggc tactgggtgg ccatgttgac gctgtactgg 1680
gtgggcgtgc ggaggctttg ccggcggcgg accgggggct accgcgtcca ggtgtga 1737

Sequence Name: SEQ ID NO:2
Length: 578 amino acids
Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg
65 70 75 80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

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Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Pro Leu Gly Leu Tyr Arg Asn Asn Leu Leu Gln Gln Phe
305 310 315 320

Leu Glu Ala Trp Tyr Asn Gln Lys Phe Leu Gly Thr His Cys Thr Phe
325 330 335

Gly Asp Asp Arg His Leu Thr Asn Arg Met Leu Ser Met Gly Tyr Ala
340 345 350

Thr Lys Tyr Thr Ser Arg Ser Arg Cys Tyr Ser Glu Thr Pro Ser Ser
355 360 365

Phe Leu Arg Trp Leu Ser Gln Gln Thr Arg Trp Ser Lys Ser Tyr Phe
370 375 380

Arg Glu Trp Leu Tyr Asn Ala Leu Trp Trp His Arg His His Ala Trp
385 390 395 400

Met Thr Tyr Glu Ala Val Val Ser Gly Leu Phe Pro Phe Phe Val Ala
405 410 415

Ala Thr Val Leu Arg Leu Phe Tyr Ala Gly Arg Pro Trp Ala Leu Leu
420 425 430

Trp Val Leu Leu Cys Val Gln Gly Val Ala Leu Ala Lys Ala Ala Phe

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435

440

445

Ala Ala Trp Leu Arg Gly Cys Leu Arg Met Val Leu Leu Ser Leu Tyr
450 455 460

Ala Pro Leu Tyr Met Cys Gly Leu Leu Pro Ala Lys Phe Leu Ala Leu
465 470 475 480

Val Thr Met Asn Gln Ser Gly Trp Gly Thr Ser Gly Arg Arg Lys Leu
485 490 495

Ala Ala Asn Tyr Val Pro Leu Leu Pro Leu Ala Leu Trp Ala Leu Leu
500 505 510

Leu Leu Gly Gly Leu Val Arg Ser Val Ala His Glu Ala Arg Ala Asp
515 520 525

Trp Ser Gly Pro Ser Arg Ala Ala Glu Ala Tyr His Leu Ala Ala Gly
530 535 540

Ala Gly Ala Tyr Val Gly Tyr Trp Val Ala Met Leu Thr Leu Tyr Trp
545 550 555 560

Val Gly Val Arg Arg Leu Cys Arg Arg Arg Thr Gly Gly Tyr Arg Val
565 570 575

Gln Val

Sequence Name: SEQ ID NO:3
Length: 1071 base pairs
Type: DNA

atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc 60
cggaggggtgc tgaccatcgc cttcgccctg ctcacatcctgg gcctcatgac ctgggcctac 120
gccgcggggg tgccgctggc ctcgcatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttccttt cagcgcacct ggtggcgcag agcctcttcg cgtacctgga gcaccggcgg 240
gtggcggcgg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccgctac ctgcgccagt gcctggcgctc cgcccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgtc ctcatggtgg tggatggcaa ccgcgccgag 420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggaccc cgccacgtac 480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cggcgggcgc ggtgggcgcc 540

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```
ggagcctatc gggaggtgga ggcggaggat cctgggcggc tggcagtgga ggcgctggtg 600
aggactcgca ggtgctgtg cgtggcgag cgctggggcg gcaagcgca ggcatgtac 660
acagccttca aggcgctcgg agattcgggtg gactacgtgc aggtctgtga ctcggaacaca 720
aggttggacc ccattggcact gctggagctc gtgcgggtac tggacgagga cccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aacctcttg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg ctgttcagag ctacttcac 900
tgtgtatcct gcatcagcgg ttctctaggt acacctccag gtcccgtgc tactcagaga 960
cgccctcgtc cttcctgcgg tggctgagcc agcagacacg ctgggtccaag tcgtacttcc 1020
gtgagtggct gtacaacgcg ctctggtggc accggcacca tgcgtggatg a 1071
```

Sequence Name: SEQ ID NO:4

Length: 376 amino acids

Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg
65 70 75 80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

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Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Ser Leu Gly Thr Pro Pro Gly Pro Ala Ala Thr Gln Arg
305 310 315 320

Arg Pro Arg Pro Ser Cys Gly Gly Ala Ser Arg His Ala Gly Pro Ser
325 330 335

Arg Thr Ser Val Ser Gly Cys Thr Thr Arg Ser Gly Gly Thr Gly Thr
340 345 350

Met Arg Gly Pro Thr Arg Arg Trp Ser Pro Ala Cys Ser Pro Ser Ser
355 360 365

Trp Arg Pro Leu Cys Cys Val Cys
370 375

Sequence Name: SEQ ID NO:5
Length: 1083 base pairs
Type: DNA

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```
atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc 60
cggaggggtgc tgaccatcgc cttcgccctg ctcacccctgg gcctcatgac ctgggcctac 120
gccgcggggg tgccgctggc ctccgatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttccttt cagcgcacct ggtggcgagc agcctcttcg cgtacctgga gcaccggcgg 240
gtggcgggcg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccgcgtag ctgcgccagt gcctggcgctc cgcccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgctc ctcattggtg tggatggcaa ccgcgcgcgag 420
gacctctaca tggctgacat gttccgcgag gtcttcgctg acgaggacct cgccacgtac 480
gtgtgggacg gcaactacca ccagccctgg gaacccgcgg cggcgggcgc ggtggggcgc 540
ggagcctatc gggaggtgga ggcggaggat cctggggcggc tggcagtgga ggcgctgggtg 600
aggactcgca ggtgcgtgtg cgtggcgagc cgctggggcg gcaagcgca ggtcatgtac 660
acagccttca aggcgctcgg agattcgggtg gactacgtgc aggtctgtga ctcgacaca 720
aggttggacc ccatggcact gctggagctc gtgcgggtac tggacgagga ccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aacctcttg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttcac 900
tgtgtatcct gcatcagcgg tcctctagaa tcctgccag gccccagga gcacgcgatg 960
atgccctcat tcctgcgcc cgtgcaggta cacctccagg tcccgctgct actcagagac 1020
gccctcgtcc ttctgcgggt ggctgagcca gcagacacgc tggccaagt cgtacttccg 1080
tga 1083
```

Sequence Name: SEQ ID NO:6
Length: 360 amino acids
Type: amino acid

Met Arg Gln Gln Asp Ala Pro Lys Pro Thr Pro Ala Ala Arg Arg Cys
1 5 10 15

Ser Gly Leu Ala Arg Arg Val Leu Thr Ile Ala Phe Ala Leu Leu Ile
20 25 30

Leu Gly Leu Met Thr Trp Ala Tyr Ala Ala Gly Val Pro Leu Ala Ser
35 40 45

Asp Arg Tyr Gly Leu Leu Ala Phe Gly Leu Tyr Gly Ala Phe Leu Ser
50 55 60

Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu Glu His Arg Arg

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65 70 75 80

Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala Thr Ala Arg Ser
85 90 95

Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro Ala Tyr Leu Arg
100 105 110

Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro Arg Ala Arg Leu
115 120 125

Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu Asp Leu Tyr Met
130 135 140

Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp Pro Ala Thr Tyr
145 150 155 160

Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro Ala Ala Ala Gly
165 170 175

Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala Glu Asp Pro Gly
180 185 190

Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg Cys Val Cys Val
195 200 205

Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr Thr Ala Phe Lys
210 215 220

Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys Asp Ser Asp Thr
225 230 235 240

Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg Val Leu Asp Glu
245 250 255

Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg Ile Leu Asn Pro
260 265 270

Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg Tyr Trp Val Ala
275 280 285

Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His Cys Val Ser Cys
290 295 300

Ile Ser Gly Pro Leu Glu Ser Cys Pro Gly Pro Arg Glu His Ala Met
305 310 315 320

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Met Pro Ser Phe Leu Ala Pro Val Gln Val His Leu Gln Val Pro Leu
325 330 335

Leu Leu Arg Asp Ala Leu Val Leu Pro Ala Val Ala Glu Pro Ala Asp
340 345 350

Thr Leu Val Gln Val Val Leu Pro
355 360

Sequence Name: SEQ ID NO:7
Length: 1065 base pairs
Type: DNA

```
atgagacagc aggacgcgcc caagcccact cctgcagccc gccgctgctc cggcctggcc 60
cggaggggtgc tgaccatcgc cttcgccttg ctcatcctgg gcctcatgac ctgggcctac 120
gccgccgggg tgccgctggc ctccgatcgc tacggcctcc tggccttcgg cctctacggg 180
gccttccttt cagcgcacct ggtggcgag agcctcttcg cgtacctgga gcaccggcgg 240
gtggcgggcg cggcgcgggg gccgctggat gcagccaccg cgcgcagtgt ggcgctgacc 300
atctccgcct accaggagga ccccgcgtag ctgcgccagt gcctggcgtc cgcccgcgcc 360
ctgctgtacc cgcgcgcgcg gctgcgcgtc ctcatggtgg tggatggcaa ccgcgccgag 420
gacctctaca tggtcgacat gttccgcgag gtcttcgctg acgaggacct cgccacgtac 480
gtgtgggacg gcaactacca ccagccctgg gaaccgcgg cggcgggcgc ggtggggcgc 540
ggagcctatc gggaggtgga ggcggaggat cctggggcggc tggcagtgga ggcgctggtg 600
aggactcgca ggtgcgtgtg cgtggcgag cgctggggcg gcaagcgca ggtcatgtac 660
acagccttca aggcgctcgg agattcggtg gactacgtgc aggtctgtga ctcggaacaca 720
aggttgagacc ccatggcact gctggagctc gtgcgggtac tggacgagga cccccgggta 780
ggggctgttg gtggggacgt gcggatcctt aaccctctgg actcctgggt cagcttccta 840
agcagcctgc gatactgggt agccttcaat gtggagcggg cttgtcagag ctacttcac 900
tgtgtatcct gcatcagcgg tcctctaggc ctatatagga ataacctctt gcagcagttt 960
cttgaggcct ggtacaacca gaagttcctg ggtaccact gtacttttgg ggatgaccgg 1020
cacctacca accgcatgct cagcatgggt tatgtacca agtaa 1065
```

Sequence Name: SEQ ID NO:8
Length: 320 amino acids
Type: PRT

Ala Phe Leu Ser Ala His Leu Val Ala Gln Ser Leu Phe Ala Tyr Leu
1 5 10 15

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Glu His Arg Arg Val Ala Ala Ala Ala Arg Gly Pro Leu Asp Ala Ala
20 25 30

Thr Ala Arg Ser Val Ala Leu Thr Ile Ser Ala Tyr Gln Glu Asp Pro
35 40 45

Ala Tyr Leu Arg Gln Cys Leu Ala Ser Ala Arg Ala Leu Leu Tyr Pro
50 55 60

Arg Ala Arg Leu Arg Val Leu Met Val Val Asp Gly Asn Arg Ala Glu
65 70 75 80

Asp Leu Tyr Met Val Asp Met Phe Arg Glu Val Phe Ala Asp Glu Asp
85 90 95

Pro Ala Thr Tyr Val Trp Asp Gly Asn Tyr His Gln Pro Trp Glu Pro
100 105 110

Ala Ala Ala Gly Ala Val Gly Ala Gly Ala Tyr Arg Glu Val Glu Ala
115 120 125

Glu Asp Pro Gly Arg Leu Ala Val Glu Ala Leu Val Arg Thr Arg Arg
130 135 140

Cys Val Cys Val Ala Gln Arg Trp Gly Gly Lys Arg Glu Val Met Tyr
145 150 155 160

Thr Ala Phe Lys Ala Leu Gly Asp Ser Val Asp Tyr Val Gln Val Cys
165 170 175

Asp Ser Asp Thr Arg Leu Asp Pro Met Ala Leu Leu Glu Leu Val Arg
180 185 190

Val Leu Asp Glu Asp Pro Arg Val Gly Ala Val Gly Gly Asp Val Arg
195 200 205

Ile Leu Asn Pro Leu Asp Ser Trp Val Ser Phe Leu Ser Ser Leu Arg
210 215 220

Tyr Trp Val Ala Phe Asn Val Glu Arg Ala Cys Gln Ser Tyr Phe His
225 230 235 240

Cys Val Ser Cys Ile Ser Gly Pro Leu Gly Leu Tyr Arg Asn Asn Leu
245 250 255

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Leu Gln Gln Phe Leu Glu Ala Trp Tyr Asn Gln Lys Phe Leu Gly Thr
260 265 270

His Cys Thr Phe Gly Asp Asp Arg His Leu Thr Asn Arg Met Leu Ser
275 280 285

Met Gly Tyr Ala Thr Lys Ala Glu Gly Thr Arg Trp Ser Gly Thr Pro
290 295 300

Pro Gly Pro Ala Ala Thr Gln Arg Arg Pro Arg Pro Ser Cys Gly Gly
305 310 315 320

Sequence Name: SEQ ID NO:9
Length: 20 base pairs
Type: DNA

cgggcttgctc agagctactt 20

Sequence Name: SEQ ID NO:10
Length: 20 base pairs
Type: DNA

agggcgtctc tgagtagcag 20

Sequence Name: SEQ ID NO:11
Length: 20 base pairs
Type: DNA

gcctcatctg tggagatggt 20

Sequence Name: SEQ ID NO:12
Length: 20 base pairs
Type: DNA

tcccagaggt ccactaatgc 20

Sequence Name: SEQ ID NO:13
Length: 20 base pairs
Type: DNA

catccaggtg tgcgactctg 20

Sequence Name: SEQ ID NO:14
Length: 20 base pairs
Type: DNA

cgctgctcag gaaggaaatc 20

Sequence Name: SEQ ID NO:15
Length: 2068
Type: DNA

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gtaagctgag gggaccaggt ggtc gatgtg tggaggccaa tgaatatcct agcgtgtgtg 60
catgctgaga gttctccaaa tccaaagtaa ctcaccagac aatgggctct atcaagttag 120
acttttagagg agagaggagg ataccataat gggcagagg gccatttgca ttgagccaat 180
ggactctacc aagttagata ttagggaaga ggggaagata ctataaggga caaggctggc 240
atttgcattg aaccatggaa tgcggtgaac tctaccaaga gaggcaagag ggtagagaat 300
tccacctaga attgagatag gagttggttc tgtcatggag accaaggtag cacagtgggg 360
agtgaagtag gaagggcaag agacaaatgg atagagtggg atctaactag tgagagagcc 420
acggagaaag aaacaagtga gagaagagga gcacctgaac tctagtaagt tcttcaagag 480
aagacaagta attccatgag actcagggga ggatgatcta gaccaagtga agttcagggg 540
agagtgattt ctgcaagcc aggtccactg aaataccag aggaaacttg ggataatcca 600
ggggaatcca tgcattaatt cactcaacaa atattcacta ggtgcctaga atgtttaagc 660
tgcggggata cagcaatagg cagacaggac accaattgat tacatcagtt ggggagacac 720
acaagaaata aataagtaga acatacagta tgttcatgat atgtgttatg gagataaata 780
atgccgggca aggggtggtg ataggaagtt ttgggggttg ggggaagt ttaagtggag 840
tgctgaagg atggggctca aggctgagaa tagtgtggct ggagcactga actgggggag 900
tattaggaga gcaggatgga gagttaagga gtggccact catgaaaggc ttataggtct 960
aaggactctg actaagatga gggagccatg ggagggtttt aagcagagaa gtgacacgtt 1020
gtaatgggat ccctctggca gccgttttgg gtacagacta caaaaggcaa ggctggaagc 1080
agggaggcca ctgaggatgc caagtgcac aggggaagga gtctggacac tgtcaagtaa 1140
tgcccaggat tctcctcttg tgtgggcttg gctggaaacc atgcagggat tgattaatga 1200
tgtctgccac aaaacaggaa ggaggcctga tggttccctt gagaagttct aatacataga 1260
ctaccctggg tagcaaccac acccatcttg ctccctccta ggctgccag taataaagca 1320
tggtagtatt agtaatatgt tagtgatagt attagtaata gtgtcagtaa ccacatgat 1380
attagtaaca gcaatagtaa tggtaacagc aatagtcata gtaaaaacgg tagtagctaa 1440
catttattga gcaataacta tctactggtc ctaagcactt ggcgtttaat ttcattcaat 1500
ccttactatc cttgtcttat gagagccttt ttttttttct tatagagtct tgctgtgttg 1560
ctcaggctca ggctggagtg caggggcacg atcatggctc actgcagcct caaactcctg 1620
agctcaagtg attccccat ctcagcctcc caaatagctg ggactacagg ccaccacgcc 1680
cggctaattt tttttttttt tttttttttt tagagatggg gtctcactat gttgcctagg 1740
ctgatctcaa actcttagcc tcaagtgatc cccctacctc agcctcctaa agtgctggga 1800

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ttacaggcat gagccattgc atccccacca ttggtgctta tttatttatt tattttattta 1860
tttagagatg gggctcttgct atgttgccca ggctgggtctt gaactcctta tccctcagcc 1920
tcccaaagtg ctgggattac aggagtgagc caccgcgtcc aggcctagga accattatcc 1980
accctattct acacatgaga aactgagggc ctagagaggt taagaaactc gccccagtg 2040
gccgtccaca gtggtcattt ctgcctcc 2068
```